

RAW SEQUENCE LISTING

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Application Serial Number: 10/579,286
Source: IFWJ
Date Processed by STIC: 5/24/06

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/579,286

DATE: 05/24/2006
TIME: 12:21:38

Input Set : A:\39618a.txt
Output Set: N:\CRF4\05242006\J579286.raw

3 <110> APPLICANT: ANDREEV, et al.
5 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF ACTIVE KIT
TYROSINE KINASE
6 RECEPTOR
8 <130> FILE REFERENCE: 30694/39618A
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,286
C--> 10 <141> CURRENT FILING DATE: 2006-05-15
10 <150> PRIOR APPLICATION NUMBER: US 60/526,930
11 <151> PRIOR FILING DATE: 2003-12-04
13 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 5084
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (22)..(2952)
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31 ctc tgc gtt ctg ctc cta ctg ctt cgc gtc cag aca ggc tct tct caa 99
32 Leu Cys Val Leu Leu Leu Leu Arg Val Gln Thr Gly Ser Ser Gln
33 15 20 25
35 cca tct gtg agt cca ggg gaa ccg tct cca cca tcc atc cat cca gga 147
36 Pro Ser Val Ser Pro Gly Glu Pro Ser Pro Pro Ser Ile His Pro Gly
37 30 35 40
39 aaa tca gac tta ata gtc cgc gtg ggc gac gag att agg ctg tta tgc 195
40 Lys Ser Asp Leu Ile Val Arg Val Gly Asp Glu Ile Arg Leu Leu Cys
41 45 50 55
43 act gat ccg ggc ttt gtc aaa tgg act ttt gag atc ctg gat gaa acg 243
44 Thr Asp Pro Gly Phe Val Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr
45 60 65 70
47 aat gag aat aag cag aat gaa tgg atc acg gaa aag gca gaa gcc acc 291
48 Asn Glu Asn Lys Gln Asn Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr
49 75 80 85 90
51 aac acc ggc aaa tac acg tgc acc aac aaa cac ggc tta agc aat tcc 339
52 Asn Thr Gly Lys Tyr Thr Cys Thr Asn Lys His Gly Leu Ser Asn Ser
53 95 100 105
55 att tat gtg ttt gtt aga gat cct gcc aag ctt ttc ctt gtt gac cgc 387
56 Ile Tyr Val Phe Val Arg Asp Pro Ala Lys Leu Phe Leu Val Asp Arg
57 110 115 120
59 tcc ttg tat ggg aaa gaa gac aac gac acg ctg gtc cgc tgt cct ctc 435

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61		125				130					135						
63	aca	gac	cca	gaa	gtg	acc	aat	tat	tcc	ctc	aag	ggg	tgc	cag	ggg	aag	483
64	Thr	Asp	Pro	Glu	Val	Thr	Asn	Tyr	Ser	Leu	Lys	Gly	Cys	Gln	Gly	Lys	
65		140				145			145		150						
67	cct	ctt	ccc	aag	gac	ttg	agg	ttt	att	cct	gac	ccc	aag	gcg	ggc	atc	531
68	Pro	Leu	Pro	Lys	Asp	Leu	Arg	Phe	Ile	Pro	Asp	Pro	Lys	Ala	Gly	Ile	
69	155					160				165		170					
71	atg	atc	aaa	agt	gtg	aaa	cgc	gcc	tac	cat	cgg	ctc	tgt	ctg	cat	tgt	579
72	Met	Ile	Lys	Ser	Val	Lys	Arg	Ala	Tyr	His	Arg	Leu	Cys	Leu	His	Cys	
73						175				180		185					
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77						190			195		200						
79	aaa	gtg	agg	cca	gcc	ttc	aaa	gct	gtg	cct	gtt	gtg	tct	gtg	tcc	aaa	675
80	Lys	Val	Arg	Pro	Ala	Phe	Lys	Ala	Val	Pro	Val	Val	Ser	Val	Ser	Lys	
81						205			210		215						
83	gca	agc	tat	ctt	ctt	agg	gaa	ggg	gaa	ttc	aca	gtg	acg	tgc	aca	723	
84	Ala	Ser	Tyr	Leu	Leu	Arg	Glu	Gly	Glu	Glu	Phe	Thr	Val	Thr	Cys	Thr	
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93						255				260		265					
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107	atc	ttc	ccc	atg	ata	aac	act	aca	gtt	ttt	gta	aac	gat	gga	gaa	aat	1011
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111	gta	gat	ttg	att	gtt	gaa	tat	gaa	gca	ttc	ccc	aaa	cct	gaa	cac	cag	1059
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119	ccc	aag	tct	gag	aat	gaa	agt	aat	atc	aga	tac	gta	agt	gaa	ttt	cat	1155
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121						365			370		375						
123	cta	acg	aga	tta	aaa	ggc	acc	gaa	gga	ggc	act	tac	aca	ttc	cta	gtg	1203
124	Leu	Thr	Arg	Leu	Lys	Gly	Thr	Glu	Gly	Gly	Thr	Tyr	Thr	Phe	Leu	Val	

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131	aca aaa cca gaa atc ctg act tac gac agg ctc gtg aat ggc atg ctc			1299
132	Thr Lys Pro Glu Ile Leu Thr Tyr Asp Arg Leu Val Asn Gly Met Leu			
133	415	420		425
135	caa tgt gtg gca gca gga ttc cca gag ccc aca ata gat tgg tat ttt			1347
136	Gln Cys Val Ala Ala Gly Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe			
137	430	435		440
139	tgt cca gga act gag cag aga tgc tct gct tct gta ctg cca gtg gat			1395
140	Cys Pro Gly Thr Glu Gln Arg Cys Ser Ala Ser Val Leu Pro Val Asp			
141	445	450		455
143	gtg cag aca cta aac tca tct ggg cca ccg ttt gga aag cta gtg gtt			1443
144	Val Gln Thr Leu Asn Ser Ser Gly Pro Pro Phe Gly Lys Leu Val Val			
145	460	465		470
147	cag agt tct ata gat tct agt gca ttc aag cac aat ggc acg gtt gaa			1491
148	Gln Ser Ser Ile Asp Ser Ser Ala Phe Lys His Asn Gly Thr Val Glu			
149	475	480	485	490
151	tgt aag gct tac aac gat gtg ggc aag act tct gcc tat ttt aac ttt			1539
152	Cys Lys Ala Tyr Asn Asp Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe			
153	495	500		505
155	gca ttt aaa ggt aac aac aaa gag caa atc cat ccc cac acc ctg ttc			1587
156	Ala Phe Lys Gly Asn Asn Lys Glu Gln Ile His Pro His Thr Leu Phe			
157	510	515		520
159	act cct ttg ctg att ggt ttc gta atc gta gct ggc atg atg tgc att			1635
160	Thr Pro Leu Leu Ile Gly Phe Val Ile Val Ala Gly Met Met Cys Ile			
161	525	530		535
163	att gtg atg att ctg acc tac aaa tat tta cag aaa ccc atg tat gaa			1683
164	Ile Val Met Ile Leu Thr Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu			
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167	gta cag tgg aag gtt gtt gag gag ata aat gga aac aat tat gtt tac			1731
168	Val Gln Trp Lys Val Val Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr			
169	555	560	565	570
171	ata gac cca aca caa ctt cct tat gat cac aaa tgg gag ttt ccc aga			1779
172	Ile Asp Pro Thr Gln Leu Pro Tyr Asp His Lys Trp Glu Phe Pro Arg			
173	575	580		585
175	aac agg ctg agt ttt ggg aaa acc ctg ggt gct gga gct ttc ggg aag			1827
176	Asn Arg Leu Ser Phe Gly Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys			
177	590	595		600
179	gtt gtt gag gca act gct tat ggc tta att aag tca gat gcg gcc atg			1875
180	Val Val Glu Ala Thr Ala Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met			
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183	act gtc gct gta aag atg ctc aag ccg agt gcc cat ttg aca gaa cgg			1923
184	Thr Val Ala Val Lys Met Leu Lys Pro Ser Ala His Leu Thr Glu Arg			
185	620	625		630
187	gaa gcc ctc atg tct gaa ctc aaa gtc ctg agt tac ctt ggt aat cac			1971
188	Glu Ala Leu Met Ser Glu Leu Lys Val Leu Ser Tyr Leu Gly Asn His			
189	635	640	645	650

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192 Met Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr	
193 655 660 665	
195 ctg gtc att aca gaa tat tgt tgc tat ggt gat ctt ttg aat ttt ttg	2067
196 Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu	
197 670 675 680	
199 aga aga aaa cgt gat tca ttt att tgt tca aag cag gaa gat cat gca	2115
200 Arg Arg Lys Arg Asp Ser Phe Ile Cys Ser Lys Gln Glu Asp His Ala	
201 685 690 695	
203 gaa gct gca ctt tat aag aat ctt ctg cat tca aag gag tct tcc tgc	2163
204 Glu Ala Ala Leu Tyr Lys Asn Leu Leu His Ser Lys Glu Ser Ser Cys	
205 700 705 710	
207 agc gat agt act aat gag tac atg gac atg aaa cct gga gtt tct tat	2211
208 Ser Asp Ser Thr Asn Glu Tyr Met Asp Met Lys Pro Gly Val Ser Tyr	
209 715 720 725 730	
211 gtt gtc cca acc aag gcc gac aaa agg aga tct gtg aga ata ggc tca	2259
212 Val Val Pro Thr Lys Ala Asp Lys Arg Arg Ser Val Arg Ile Gly Ser	
213 735 740 745	
215 tac ata gaa aga gat gtg act ccc gcc atc atg gag gat gac gag ttg	2307
216 Tyr Ile Glu Arg Asp Val Thr Pro Ala Ile Met Glu Asp Asp Glu Leu	
217 750 755 760	
219 gcc cta gac tta gaa gac ttg ctg agc ttt tct tac cag gtg gca aag	2355
220 Ala Leu Asp Leu Glu Asp Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys	
221 765 770 775	
223 ggc atg gct ttc ctc gcc tcc aag aat tgt att cac aga gac ttg gca	2403
224 Gly Met Ala Phe Leu Ala Ser Lys Asn Cys Ile His Arg Asp Leu Ala	
225 780 785 790	
227 gcc aga aat atc ctc ctt act cat ggt cggt atc aca aag att tgt gat	2451
228 Ala Arg Asn Ile Leu Leu Thr His Gly Arg Ile Thr Lys Ile Cys Asp	
229 795 800 805 810	
231 ttt ggt cta gcc aga gac atc aag aat gat tct aat tat gtg gtt aaa	2499
232 Phe Gly Leu Ala Arg Asp Ile Lys Asn Asp Ser Asn Tyr Val Val Lys	
233 815 820 825	
235 gga aac gct cga cta cct gtg aag tgg atg gca cct gaa agc att ttc	2547
236 Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe	
237 830 835 840	
239 aac tgt gta tac acg ttt gaa agt gac gtc tgg tcc tat ggg att ttt	2595
240 Asn Cys Val Tyr Thr Phe Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe	
241 845 850 855	
243 ctt tgg gag ctg ttc tct tta gga agc agc ccc tat cct gga atg ccg	2643
244 Leu Trp Glu Leu Phe Ser Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro	
245 860 865 870	
247 gtc gat tct aag ttc tac aag atg atc aag gaa ggc ttc cggt atg ctc	2691
248 Val Asp Ser Lys Phe Tyr Lys Met Ile Lys Glu Gly Phe Arg Met Leu	
249 875 880 885 890	
251 agc cct gaa cac gca cct gct gaa atg tat gac ata atg aag act tgc	2739
252 Ser Pro Glu His Ala Pro Ala Glu Met Tyr Asp Ile Met Lys Thr Cys	
253 895 900 905	
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260	Leu	Ile	Glu	Lys	Gln	Ile	Ser	Glu	Ser	Thr	Asn	His	Ile	Tyr	Ser	Asn	
261																	
263	925																2883
264	tta	gca	aac	tgc	agc	ccc	aac	cga	cag	aag	ccc	gtg	gta	gac	cat	tct	
265	Leu	Ala	Asn	Cys	Ser	Pro	Asn	Arg	Gln	Lys	Pro	Val	Val	Asp	His	Ser	
266	940																
267	gtg	cgg	atc	aat	tct	gtc	ggc	agc	acc	gct	tcc	tcc	tcc	cag	cct	ctg	
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date